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p#13

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TECH CENTER 1600/2900

RAW SEQUENCE LISTING

DATE: 07/05/2001

PATENT APPLICATION: US/09/138,735

TIME: 11:22:57

Input Set : A:\PTO.txt

Output Set: N:\CRF3\07052001\I138735.raw

3 <110> APPLICANT: PARANHOS-BACCALA, Glaucia
 4 LESENECHAL, Mylene
 5 JOLIVET, Michel
 7 <120> TITLE OF INVENTION: TRYPANOSOMA CRUZI ANTIGEN, GENE ENCODING THEREFOR AND
 METHODS OF
 8 DETECTING AND TREATING CHAGAS DISEASE
 10 <130> FILE REFERENCE: WPB 36400B
 12 <140> CURRENT APPLICATION NUMBER: US 09/138,735
 13 <141> CURRENT FILING DATE: 1998-08-24
 15 <150> PRIOR APPLICATION NUMBER: US 08/480,917
 16 <151> PRIOR FILING DATE: 1995-06-07
 18 <150> PRIOR APPLICATION NUMBER: FR 94/10132
 19 <151> PRIOR FILING DATE: 1994-08-12
 21 <160> NUMBER OF SEQ ID NOS: 13
 23 <170> SOFTWARE: PatentIn version 3.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 3402
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Trypanosoma cruzi
 30 <400> SEQUENCE: 1

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33	gaagtacttg	ccgttttgtg	tgggtgacga	gacaacacac	atcgagcggg	aagaaaaaaa	120
35	aaaaggaaat	aaattaaatt	aaattatttg	ttctttgaat	aggcaaagaa	gaagaagaag	180
37	aaaagggtgcg	ggggagggag	gagaaagcga	cacacacaca	aaaaaaaaaa	aaggaattgc	240
39	ggaaataaca	acgcaaggcg	cggacatgac	cgtgacggtg	gatttgttca	atcatgcgaa	300
41	gccgagcaac	aatgagggcc	gcgtgtggtc	tgtggacgcc	gcgacattta	acgaggtgcc	360
43	tgaggcgag	cgtgtgctgg	cggattcgca	gttttatctt	gcctacacca	tgaagcgggc	420
45	tcacgtgctg	cgtgtggtga	agcgctcgaa	ccttttgaag	ggcaccgtgc	gggcacactc	480
47	aaagcccatt	catgcggtga	agtttgtgaa	ttaccgcagt	aacgtcgag	catcggtg	540
49	gaagggggag	ttcttcgtgt	gggttgtgac	ggatgaaacg	gaggcgagca	acggcaagcc	600
51	ggatctcgca	gcccgcctca	cagtgaaggt	gtactttaag	cttcaggatc	ctgtcacaat	660
53	tccatgcttt	tctttcttta	tcaacgcga	gagtcagcgg	cctgatctgc	ttgtccttta	720
55	cgaaacgcag	gcggcaattc	ttgacagctc	ctccctcatt	gagcgctttg	acgtggaatc	780
57	actggaggca	acactacagc	ggaattgcac	aacctgcca	acctgactc	aaccggttag	840
59	tgagaacagt	ttatgctccg	ttggctctgg	cggatggttc	acctttacca	cggaaaccaac	900
61	aatggtagcg	gcatgcacat	tacgaaaccg	cagcactcca	tcatgggcgt	gttgcgaggg	960
63	tgagccagtg	aaggcattgc	atctccttga	cgcaaccggt	gaggaaaatg	tcagtgttct	1020
65	cgtggccgca	tctacaaaag	gggtgtacca	atggctcctt	acgggtgtag	cagaaccaa	1080
67	cttggtgcgc	aagtttgtca	ttgatggatc	tattgtcgcg	atggaaagct	cacgagaaac	1140
69	gtttgcggtg	tttgacgaca	ggaagcagct	ggcgctggtc	aacatgcatt	cccctcataa	1200
71	ctttacctgc	acacactaca	tgatgccttg	tcaggtacag	cgtaacggct	tttgcttcaa	1260
73	tcgtacagcc	gacggtagct	gcgtcctggc	tgacatgtcg	attcgattga	cgatcttcca	1320
75	tctccggtcc	tcccgcaggg	aagaacagca	gccaggccaa	aaaacatcgg	tagtggcgac	1380
77	ggcgaaaccg	gggtgtgtgt	cctcgggcac	tgacgcggcg	agtagcagtc	ataccaatac	1440
79	gacttctgcc	gctgctgcat	cccctgcate	acccctgtt	tcagcgccag	ccaaggcagc	1500
81	cgcgctctct	gcccgcggcg	gatcggtga	gccgcacgtg	gggagcaaga	tcattgctaa	1560
83	tctagtgaat	cagctgggga	ttaatgtcac	ccaaaggagc	gtcgtcagca	ctggagcgcc	1620
85	ggccacgacg	aggtctacgg	cggtgacgtc	cacgactacc	gccccgcagc	gaacaagtcc	1680

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87 atacggggcac aatggccgac ctgtgacggc tggattggtg gcagctaata gtggtgccag 1740
89 cgcggcctcg tctcccacag ccgcggcgaa accaacagga gaagaaaagg cctccgcggc 1800
91 atgtgaaacg agctccgtgg cgataaatgc gacacgcccg gcgcttcaca acgcctctct 1860
93 cccgcaggcg ccaacggatg gcgttttggc ggcagcagta taccagtcgg agggcgaggt 1920
95 tcatcagtcg ctggagcggc tggagtcogt cataaccaac acgtctcggg ttctgaagtt 1980
97 gctccctgac accattcgaa gagaccatga acaacttctg aatctgggtt tagaggcaca 2040
99 gatgacagag ctgcagcaga gccgtccaac accgcaaaca cagccgagag acacaagctc 2100
101 cgcgaaatca tccgtgtttg agacgtacac ccttgttctc attgcggatt ccctctctcg 2160
103 caacatcacg aagggggtga agcgtggtgt gaacgaggcc attatgttgc atctcgacca 2220
105 tgaggtgcgg cacgccatag ggaaccggct tcggcaaaca caaaagaaca tcatcaagag 2280
107 ccgcctcgat gaagcgttga aggaagcac tacacagttt acggctcaat tgacgcaaac 2340
109 ggtggagaat ctggtgaagc gcgagcttgc cgaggtgctt ggtagcatca acggctccct 2400
111 cacttctctc gtgaaggaaa atgcctcatt acagaaagag ttgaattcca taatgtctag 2460
113 tggggtgttg gatgaaatgc gtctgatgcg ggaagagctg tgcacattgc gagagtccgt 2520
115 tgcgaagcgg aaggcaacaa tgccagattc ttctcttcac gccacgagct cctttcaagg 2580
117 aagaaggtct gcgcccagaga caattcttgc aaccgcgtta tcgatggtgc gagagcagca 2640
119 ataccgtcag ggactggaat acatgttgat ggctcagcag ccctctctcc tctgcgggtt 2700
121 cctcagcata cttacaaggg aaaacgaaaa cgctactcgc gaacttattg aaaatgtaga 2760
123 gacgccgaat gacgtgtggt gttcggttct gttgcaactc atagaggccg cggcgaccga 2820
125 ggctgagaag gaggtggttg ttggcgtcgc cattgatatt ctctccgagc gcgatcaaat 2880
127 tgctcagaac ggcgcaactc gctcgaaact caccaccgcc atgcgagcct ttgagcgaca 2940
129 ggcaaggtcg gagacaacga gcaggtcatt cttgcaatgc ctgaagaacc tggaaaagct 3000
131 tctgcaatca tgataataaa aagaactcaa cgaatacagt tgttgattat taaggaaggg 3060
133 aaaagagaga aagagagaga gagagagaga aatgtaatgg gcgtttagtt acggtagaaa 3120
135 gaaaacgtgt ggataagaag gaggggtttt gtgtgcgacc aggaattact ggggaacgct 3180
137 gctacacggc ggaatcgacc attttattat tattattatt gtctttagta ttatgttttt 3240
139 tcttgtgtgt gtgtgtgtgt gtttgtgtgt gtgcggttat tttgtatccg tttgctcccg 3300
141 cccctgcccc ccatcaccgc aggagaaagt agaataagac acatacgatt gttgtttttg 3360
143 ttatccttaa aaggaagaga gaccaaaaaa aaaaaaaaaa aa 3402

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146 <210> SEQ ID NO: 2

147 <211> LENGTH: 915

148 <212> TYPE: PRT

149 <213> ORGANISM: Trypanosoma cruzi

151 <400> SEQUENCE: 2

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153 Met Thr Val Thr Val Asp Leu Phe Asn His Ala Lys Pro Ser Asn Asn
154 1 5 10 15
156 Glu Gly Arg Val Trp Ser Val Asp Ala Ala Thr Phe Asn Glu Val Pro
157 20 25 30
159 Glu Ala Gln Arg Val Leu Ala Asp Ser Gln Phe Tyr Leu Ala Tyr Thr
160 35 40 45
162 Met Lys Arg Arg His Val Leu Arg Val Val Lys Arg Ser Asn Leu Leu
163 50 55 60
165 Lys Gly Thr Val Arg Ala His Ser Lys Pro Ile His Ala Val Lys Phe
166 65 70 75 80
168 Val Asn Tyr Arg Ser Asn Val Ala Ala Ser Ala Gly Lys Gly Glu Phe
169 85 90 95
171 Phe Val Trp Val Val Thr Asp Glu Thr Asp Ala Ser Asn Gly Lys Pro
172 100 105 110
174 Asp Leu Ala Ala Arg Leu Thr Val Lys Val Tyr Phe Lys Leu Gln Asp

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175	115	120	125
177 Pro Val Thr Ile Pro Cys Phe Ser Phe Phe Ile Asn Ala Glu Ser Gln			
178 130	135	140	
180 Arg Pro Asp Leu Leu Val Leu Tyr Glu Thr Gln Ala Ala Ile Leu Asp			
181 145	150	155	160
183 Ser Ser Ser Leu Ile Glu Arg Phe Asp Val Glu Ser Leu Glu Ala Thr			
184 165	170	175	
186 Leu Gln Arg Asn Cys Thr Thr Leu Arg Thr Leu Thr Gln Pro Val Ser			
187 180	185	190	
189 Glu Asn Ser Leu Cys Ser Val Gly Ser Gly Gly Trp Phe Thr Phe Thr			
190 195	200	205	
192 Thr Glu Pro Thr Met Val Ala Ala Cys Thr Leu Arg Asn Arg Ser Thr			
193 210	215	220	
195 Pro Ser Trp Ala Cys Cys Glu Gly Glu Pro Val Lys Ala Leu His Leu			
196 225	230	235	240
198 Leu Asp Ala Thr Val Glu Glu Asn Val Ser Val Leu Val Ala Ala Ser			
199 245	250	255	
201 Thr Lys Gly Val Tyr Gln Trp Leu Leu Thr Gly Val Ala Glu Pro Asn			
202 260	265	270	
204 Leu Leu Arg Lys Phe Val Ile Asp Gly Ser Ile Val Ala Met Glu Ser			
205 275	280	285	
207 Ser Arg Glu Thr Phe Ala Val Phe Asp Asp Arg Lys Gln Leu Ala Leu			
208 290	295	300	
210 Val Asn Met His Ser Pro His Asn Phe Thr Cys Thr His Tyr Met Met			
211 305	310	315	320
213 Pro Cys Gln Val Gln Arg Asn Gly Phe Cys Phe Asn Arg Thr Ala Asp			
214 325	330	335	
216 Gly Ser Cys Val Leu Ala Asp Met Ser Asn Arg Leu Thr Ile Phe His			
217 340	345	350	
219 Leu Arg Cys Ser Arg Arg Glu Glu Gln Gln Pro Gly Gln Lys Thr Ser			
220 355	360	365	
222 Val Val Ala Thr Ala Lys Pro Gly Cys Val Ser Ser Gly Thr Asp Ala			
223 370	375	380	
225 Ala Ser Ser Ser His Thr Asn Thr Thr Ser Ala Ala Ala Ala Ser Pro			
226 385	390	395	400
228 Ala Ser Pro Pro Val Ser Ala Pro Ala Lys Ala Ala Ala Pro Pro Ala			
229 405	410	415	
231 Ala Ala Arg Ser Ala Glu Pro His Val Gly Ser Lys Ile Ile Ala Asn			
232 420	425	430	
234 Leu Val Asn Gln Leu Gly Ile Asn Val Thr Gln Arg Ser Val Val Ser			
235 435	440	445	
237 Thr Gly Ala Pro Ala Thr Thr Arg Ser Thr Ala Val Thr Ser Thr Thr			
238 450	455	460	
240 Thr Ala Pro Gln Arg Thr Ser Pro Tyr Gly His Asn Gly Arg Pro Val			
241 465	470	475	480
243 Thr Ala Gly Leu Val Ala Ala Asn Ser Gly Ala Ser Ala Ala Ser Ser			
244 485	490	495	
246 Pro Thr Ala Ala Ala Lys Pro Thr Gly Glu Glu Lys Ala Ser Ala Ala			
247 500	505	510	

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249 Cys Glu Thr Ser Ser Val Ala Ile Asn Ala Thr Arg Pro Ala Leu His
250      515      520      525
252 Asn Ala Ser Leu Pro Gln Ala Pro Thr Asp Gly Val Leu Ala Ala Ala
253      530      535      540
255 Val Tyr Gln Ser Glu Gly Glu Val His Gln Ser Leu Glu Arg Leu Glu
256 545      550      555      560
258 Ser Val Ile Thr Asn Thr Ser Arg Val Leu Lys Leu Leu Pro Asp Thr
259      565      570      575
261 Ile Arg Arg Asp His Glu Gln Leu Leu Asn Leu Gly Leu Glu Ala Gln
262      580      585      590
264 Met Thr Glu Leu Gln Gln Ser Arg Pro Thr Pro Gln Thr Gln Pro Arg
265      595      600      605
267 Asp Thr Ser Ser Ala Lys Ser Ser Val Phe Glu Thr Tyr Thr Leu Val
268      610      615      620
270 Leu Ile Ala Asp Ser Leu Ser Arg Asn Ile Thr Lys Gly Val Lys Arg
271 625      630      635      640
273 Gly Val Asn Glu Ala Ile Met Leu His Leu Asp His Glu Val Arg His
274      645      650      655
276 Ala Ile Gly Asn Arg Leu Arg Gln Thr Gln Lys Asn Ile Ile Lys Ser
277      660      665      670
279 Arg Leu Asp Glu Ala Leu Lys Glu Ser Thr Thr Gln Phe Thr Ala Gln
280      675      680      685
282 Leu Thr Gln Thr Val Glu Asn Leu Val Lys Arg Glu Leu Ala Glu Val
283      690      695      700
285 Leu Gly Ser Ile Asn Gly Ser Leu Thr Ser Leu Val Lys Glu Asn Ala
286 705      710      715      720
288 Ser Leu Lys Lys Glu Leu Asn Ser Ile Met Ser Ser Gly Val Leu Asp
289      725      730      735
291 Glu Met Arg Arg Met Arg Glu Glu Leu Cys Thr Leu Arg Glu Ser Val
292      740      745      750
294 Ala Lys Arg Lys Ala Thr Met Pro Asp Ser Ser Leu His Ala Thr Ser
295      755      760      765
297 Ser Phe Gln Gly Arg Arg Ser Ala Pro Glu Thr Ile Leu Ala Thr Ala
298      770      775      780
300 Leu Ser Met Val Arg Glu Gln Gln Tyr Arg Gln Gly Leu Glu Val Met
301 785      790      795      800
303 Leu Met Ala Gln Gln Pro Ser Leu Leu Leu Arg Phe Leu Ser Ile Leu
304      805      810      815
306 Thr Arg Glu Asn Glu Asn Ala Tyr Ser Glu Leu Ile Glu Asn Val Glu
307      820      825      830
309 Thr Pro Asn Asp Val Trp Cys Ser Val Leu Leu Gln Leu Ile Glu Ala
310      835      840      845
312 Ala Ala Thr Glu Ala Glu Lys Glu Val Val Val Gly Val Ala Ile Asp
313      850      855      860
315 Ile Leu Ser Glu Arg Asp Gln Ile Ala Gln Asn Gly Ala Leu Gly Ser
316 865      870      875      880
318 Lys Leu Thr Thr Ala Met Arg Ala Phe Glu Arg Gln Ala Arg Ser Glu
319      885      890      895
321 Thr Thr Ser Arg Ser Phe Leu Gln Cys Leu Lys Asn Leu Ile Lys Leu

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322          900          905          910
324 Leu Gln Ser
325          915
327 <210> SEQ ID NO: 3
328 <211> LENGTH: 24
329 <212> TYPE: DNA
C--> 330 <213> ORGANISM: Artificial
332 <220> FEATURE:
333 <223> OTHER INFORMATION: phage DNA primer
335 <400> SEQUENCE: 3
336 ggtggcgacg actcctggag cccg                24
339 <210> SEQ ID NO: 4
340 <211> LENGTH: 24
341 <212> TYPE: DNA
C--> 342 <213> ORGANISM: Artificial
344 <220> FEATURE:
345 <223> OTHER INFORMATION: phage DNA primer
347 <400> SEQUENCE: 4
348 ttgacaccag accaactggt aatg                24
351 <210> SEQ ID NO: 5
352 <211> LENGTH: 18
353 <212> TYPE: DNA
C--> 354 <213> ORGANISM: Artificial
356 <220> FEATURE:
357 <223> OTHER INFORMATION: primer
359 <400> SEQUENCE: 5
360 tcgggcactg acgcggcg                18
363 <210> SEQ ID NO: 6
364 <211> LENGTH: 24
365 <212> TYPE: DNA
C--> 366 <213> ORGANISM: Artificial
368 <220> FEATURE:
369 <223> OTHER INFORMATION: phage lambda gt10 DNA primer
371 <400> SEQUENCE: 6
372 cttatgagta tttcttccag ggta                24
375 <210> SEQ ID NO: 7
376 <211> LENGTH: 21
377 <212> TYPE: DNA
C--> 378 <213> ORGANISM: Artificial
380 <220> FEATURE:
381 <223> OTHER INFORMATION: probe/primer
383 <400> SEQUENCE: 7
384 aacgctatta ttagaacagt t                21
387 <210> SEQ ID NO: 8
388 <211> LENGTH: 18
389 <212> TYPE: DNA
C--> 390 <213> ORGANISM: Artificial
392 <220> FEATURE:
393 <223> OTHER INFORMATION: probe/primer

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VERIFICATION SUMMARY

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Input Set : A:\PTO.txt

Output Set: N:\CRF3\07052001\I138735.raw

L:330 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:342 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:354 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
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